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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/713,572

DATE: 05/17/2002

TIME: 09:26:44

Input Set : N:\Crf3\05132002\I713572.raw

Output Set: N:\CRF3\05172002\I713572.raw

1 <110> APPLICANT: Giuliano, Kenneth A.  
 2 Bright, Gary  
 3 Olson, Keith  
 4 Burroughs-Tencza, Sarah  
 5 <120> TITLE OF INVENTION: A System for Cell Based Screening  
 6 <130> FILE REFERENCE: 97-022-K2  
 7 <140> CURRENT APPLICATION NUMBER: US/09/713,572  
 8 <141> CURRENT FILING DATE: 2000-11-15  
 9 <150> PRIOR APPLICATION NUMBER: 09/430,656  
 10 <151> PRIOR FILING DATE: 1999-10-29  
 11 <150> PRIOR APPLICATION NUMBER: 09/398,965  
 12 <151> PRIOR FILING DATE: 1999-09-17  
 13 <150> PRIOR APPLICATION NUMBER: 09/031,271  
 14 <151> PRIOR FILING DATE: 1998-02-27  
 15 <150> PRIOR APPLICATION NUMBER: 08/810,983  
 16 <151> PRIOR FILING DATE: 1997-02-27  
 17 <150> PRIOR APPLICATION NUMBER: 60/136,078  
 18 <151> PRIOR FILING DATE: 1999-05-26  
 19 <150> PRIOR APPLICATION NUMBER: 60/106,308  
 20 <151> PRIOR FILING DATE: 1998-10-30  
 21 <160> NUMBER OF SEQ ID NOS: 168  
 22 <170> SOFTWARE: PatentIn Ver. 2.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1770  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Artificial Sequence  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (1)..(882)  
 31 <220> FEATURE:  
 32 <223> OTHER INFORMATION: Description of Artificial Sequence:  
 33 GFP-DEVD-Annexin II construct  
 34 <400> SEQUENCE: 1  
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 36 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 37 1 5 10 15  
 38 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 39 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 40 20 25 30  
 41 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 42 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 43 35 40 45  
 44 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192

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45	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
46		50					55					60					
47	ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
48	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
49	65					70					75					80	
50	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
51	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
52					85					90					95		
53	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
54	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
55				100					105					110			
56	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
57	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
58			115					120					125				
59	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
60	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
61		130					135					140					
62	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
63	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
64	145					150					155					160	
65	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
66	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
67					165					170					175		
68	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576
69	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
70			180						185					190			
71	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	624
72	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
73			195					200					205				
74	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
75	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
76		210					215				220						
77	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc	720
78	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
79		225				230					235				240		
80	gga	ctc	aga	tct	ggc	gcc	ggc	gct	gga	gcc	gga	gct	ggc	gcc	gga	gcc	768
81	Gly	Leu	Arg	Ser	Gly	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Gly	Ala	
82					245					250					255		
83	gac	gag	gtg	gac	ggc	gcc	ggc	gcc	gat	gaa	gta	gat	ggc	gcc	atg	tct	816
84	Asp	Glu	Val	Asp	Gly	Ala	Gly	Ala	Asp	Glu	Val	Asp	Gly	Ala	Met	Ser	
85			260						265					270			
86	act	gtc	cac	gaa	atc	ctg	tgc	aag	ctc	agc	ttg	gag	ggt	gat	cat	tct	864
87	Thr	Val	His	Glu	Ile	Leu	Cys	Lys	Leu	Ser	Leu	Glu	Gly	Asp	His	Ser	
88		275					280						285				
89	aca	ccc	cca	agt	gcc	tat	tgaatggtga	gcaagggcga	ggagctgttc								912
90	Thr	Pro	Pro	Ser	Ala	Tyr											
91		290															
92	accggggtgg	tgcccatcct	ggtcgagctg	gacggcgacg	taaacggcca	caagttcagc											972
93	gtgtccggcg	agggcgaggg	cgatgccacc	tacggcaagc	tgaccctgaa	gttcatctgc											1032

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94      accaccggca agctgcccggt gccctggccc accctcgtga ccaccctgac ctacggcggtg 1092
95      cagtgtttca gccgctaccc cgaccacatg aagcagcacg actttcttcaa gtccgccaatg 1152
96      cccgaaggct acgtccagga gcgcaccatc ttcttcaagg acgacggcaa ctacaagacc 1212
97      cgcgccgagg tgaagttcga gggcgacacc ctggtgaacc gcatcgagct gaagggcatc 1272
98      gacttcaagg aggacggcaa catcctgggg cacaagctgg agtacaacta caacagccac 1332
99      aacgtctata tcatggccga caagcagaag aacggcatca aggtgaactt caagatccgc 1392
100     cacaacatcg aggacggcag cgtgcagctc gccgaccact accagcagaa caccctcatc 1452
101     ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcaccagtc cgccctgagc 1512
102     aaagacccca acgagaagcg gcatcacatg gtccgtgctgg agttcgtgac cgccgcccggg 1572
103     atcactctcg gcatggacga gctgtacaag tccggactca gatctggcgc cgccgctgga 1632
104     gccggagctg gcgccggagc cgacgaggtg gacggcgccg gcgccgatga agtagatggc 1692
105     gccatgtcta ctgtccacga aatcctgtgc aagctcagct tggagggtga tcattctaca 1752
106     cccccaagtg cctattga                                     1770

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108 &lt;210&gt; SEQ ID NO: 2

109 &lt;211&gt; LENGTH: 294

110 &lt;212&gt; TYPE: PRT

111 &lt;213&gt; ORGANISM: Artificial Sequence

112 &lt;220&gt; FEATURE:

113 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:

114 GFP-DEVD-Annexin II construct

115 &lt;400&gt; SEQUENCE: 2

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116     Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
117         1           5           10           15
118     Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
119         20          25          30
120     Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
121         35          40          45
122     Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
123         50          55          60
124     Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
125         65          70          75          80
126     Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
127         85          90          95
128     Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
129         100         105         110
130     Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
131         115         120         125
132     Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
133         130         135         140
134     Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
135         145         150         155         160
136     Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
137         165         170         175
138     Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
139         180         185         190
140     Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
141         195         200         205
142     Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
143         210         215         220

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144 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
145 225 230 235 240
146 Gly Leu Arg Ser Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala
147 245 250 255
148 Asp Glu Val Asp Gly Ala Gly Ala Asp Glu Val Asp Gly Ala Met Ser
149 260 265 270
150 Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp His Ser
151 275 280 285
152 Thr Pro Pro Ser Ala Tyr
153 290
155 <210> SEQ ID NO: 3
156 <211> LENGTH: 2439
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <221> NAME/KEY: CDS
161 <222> LOCATION: (1)..(2436)
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Description of Artificial Sequence:
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165 <400> SEQUENCE: 3
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168 1 5 10 15
169 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
170 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
171 20 25 30
172 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
173 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
174 35 40 45
175 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
176 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
177 50 55 60
178 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
179 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
180 65 70 75 80
181 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
182 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
183 85 90 95
184 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
185 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
186 100 105 110
187 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
188 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
189 115 120 125
190 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
191 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
192 130 135 140
193 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480

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194	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
195	145					150					155					160	
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197	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
198					165					170					175		
199	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576
200	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
201				180					185					190			
202	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	624
203	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	
204			195					200					205				
205	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
206	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
207		210				215						220					
208	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	aag	720
209	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Lys	
210	225				230					235						240	
211	gga	gac	gaa	gtg	gac	gga	gcc	gac	ctc	agt	ctt	gtg	gat	gcg	ttg	aca	768
212	Gly	Asp	Glu	Val	Asp	Gly	Ala	Asp	Leu	Ser	Leu	Val	Asp	Ala	Leu	Thr	
213				245					250					255			
214	gaa	cca	cct	cca	gaa	att	gag	gga	gaa	ata	aag	cga	gac	ttc	atg	gct	816
215	Glu	Pro	Pro	Pro	Glu	Ile	Glu	Gly	Glu	Ile	Lys	Arg	Asp	Phe	Met	Ala	
216			260					265						270			
217	gcg	ctg	gag	gca	gag	ccc	tat	gat	gac	atc	gtg	gga	gaa	act	gtg	gag	864
218	Ala	Leu	Glu	Ala	Glu	Pro	Tyr	Asp	Ile	Val	Gly	Glu	Thr	Val	Glu		
219		275				280						285					
220	aaa	act	gag	ttt	att	cct	ctc	ctg	gat	ggt	gat	gag	aaa	acc	ggg	aac	912
221	Lys	Thr	Glu	Phe	Ile	Pro	Leu	Leu	Asp	Gly	Asp	Glu	Lys	Thr	Gly	Asn	
222		290				295					300						
223	tca	gag	tcc	aaa	aag	aaa	ccc	tgc	tta	gac	act	agc	cag	gtt	gaa	ggt	960
224	Ser	Glu	Ser	Lys	Lys	Lys	Pro	Cys	Leu	Asp	Thr	Ser	Gln	Val	Glu	Gly	
225	305				310					315					320		
226	atc	cca	tct	tct	aaa	cca	aca	ctc	cta	gcc	aat	ggt	gat	cat	gga	atg	1008
227	Ile	Pro	Ser	Ser	Lys	Pro	Thr	Leu	Leu	Ala	Asn	Gly	Asp	His	Gly	Met	
228				325						330					335		
229	gag	ggg	aat	aac	act	gca	ggg	tct	cca	act	gac	ttc	ctt	gaa	gag	aga	1056
230	Glu	Gly	Asn	Asn	Thr	Ala	Gly	Ser	Pro	Thr	Asp	Phe	Leu	Glu	Glu	Arg	
231			340					345					350				
232	gtg	gac	tat	ccg	gat	tat	cag	agc	agc	cag	aac	tgg	cca	gaa	gat	gca	1104
233	Val	Asp	Tyr	Pro	Asp	Tyr	Gln	Ser	Ser	Gln	Asn	Trp	Pro	Glu	Asp	Ala	
234			355					360					365				
235	agc	ttt	tgt	ttc	cag	cct	cag	caa	gtg	tta	gat	act	gac	cag	gct	gag	1152
236	Ser	Phe	Cys	Phe	Gln	Pro	Gln	Gln	Val	Leu	Asp	Thr	Asp	Gln	Ala	Glu	
237		370				375						380					
238	ccc	ttt	aac	gag	cac	cgt	gat	gat	ggt	ttg	gca	gat	ctg	ctc	ttt	gtc	1200
239	Pro	Phe	Asn	Glu	His	Arg	Asp	Asp	Gly	Leu	Ala	Asp	Leu	Leu	Phe	Val	
240	385				390					395					400		
241	tcc	agt	gga	ccc	acg	aac	gct	tct	gca	ttt	aca	gag	cga	gac	aat	cct	1248
242	Ser	Ser	Gly	Pro	Thr	Asn	Ala	Ser	Ala	Phe	Thr	Glu	Arg	Asp	Asn	Pro	

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